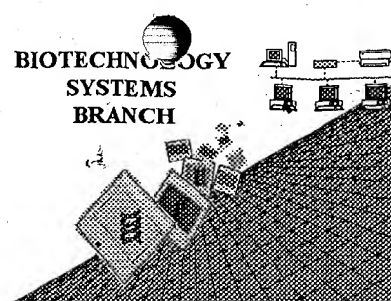


## **RAW SEQUENCE LISTING ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/773,307

Source: OIPE

Date Processed by STIC: 10/19/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/773,307

DATE: 10/19/2001

TIME: 14:05:54

Input Set : A:\pbm37seq.txt

Output Set: N:\CRF3\10192001\I773307.raw

Does Not Comply  
Corrected Diskette Needed

pp 1-3

4 <110> APPLICANT: BML, INC.  
 6 <120> TITLE OF INVENTION: Method of Detecting Risk Factor for Onset of Diabetes  
 8 <130> FILE REFERENCE: PBM37  
 10 <140> CURRENT APPLICATION NUMBER: US/09/773,307  
 11 <141> CURRENT FILING DATE: 2001-01-31  
 E--> 13 <160> NUMBER OF SEQ ID NOS: 23 22 shown (p3)  
 15 <170> SOFTWARE: PatentIn Ver. 2.0

## ERRORED SEQUENCES

17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 1305 1411  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Hominidae  
 22 <220> FEATURE:  
 23 <221> NAME/KEY: CDS  
 24 <222> LOCATION: (1)..(900)  
 26 <400> SEQUENCE: 1

E--> 28 ~~delete~~ -103 aaa cagaagggga ggtgcagttt cagaacccag ccagcctctc 61 43  
 E--> 30 tcttgcgtgca tagcctcctg ccggcctcat cttgccttag ccaaccccgct ctggagccct 1 103  
 E--> 33 atg gcc aac tgc gag ttc agc ccg gtg tcc ggg gac aaa ccc tgc tgc 48  
 34 Met Ala Asn Cys Glu Phe Ser Pro Val Ser Gly Asp Lys Pro Cys Cys  
 35 1 5 10 15  
 E--> 37 cgg ctc tct agg aga gcc caa ctc tgt ctt ggc gtc agt atc ctg gtc 96  
 38 Arg Leu Ser Arg Ala Gln Leu Cys Leu Gly Val Ser Ile Leu Val  
 39 20 25 30  
 E--> 41 ctg atc ctc gtc gtg gtg ctc gcg gtg gtc gtc ccg agg tgg cgc cag 144  
 42 Leu Ile Leu Val Val Val Leu Ala Val Val Val Pro Arg Trp Arg Gln  
 43 35 40 45  
 E--> 45 cag tgg agc ggt ccg gcc acc acc aag cgc ttt ccc gag acc gtc ctg 192  
 46 Gln Trp Ser Gly Pro Gly Thr Thr Lys Arg Phe Pro Glu Thr Val Leu  
 47 50 55 60  
 E--> 49 gcg cga tgc gtc aag tac act gaa att cat cct gag atg aga cat gta 240  
 50 Ala Arg Cys Val Lys Tyr Thr Glu Ile His Pro Glu Met Arg His Val  
 51 65 70 75 80  
 E--> 53 gac tgc caa agt gta tgg gat gct ttc aag ggt gca ttt att tca aaa 288  
 54 Asp Cys Gln Ser Val Trp Asp Ala Phe Lys Gly Ala Phe Ile Ser Lys  
 55 85 90 95  
 E--> 57 cat cct tgc aac att act gaa gaa gac tat cag cca cta atg aag ttg 336  
 58 His Pro Cys Asn Ile Thr Glu Glu Asp Tyr Gln Pro Leu Met Lys Leu  
 59 100 105 110  
 E--> 61 gga act cag acc gta cct tgc aac aag att ctt ctt tgg agc aga ata 384  
 62 Gly Thr Gln Thr Val Pro Cys Asn Lys Ile Leu Leu Trp Ser Arg Ile  
 63 115 120 125  
 E--> 65 aaa gat ctg gcc cat cag ttc aca cag gtc cag cgg gac atg ttc acc 432  
 66 Lys Asp Leu Ala His Gln Phe Thr Gln Val Gln Arg Asp Met Phe Thr

Per 1.822(c)(6) of  
 sequence rules, "The  
 enumeration of nucleotide  
 bases shall start at the first  
 base of the sequence with number 1."  
 Invalid do not use  
 negative nos.

nos.  
 off

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/773,307

DATE: 10/19/2001

TIME: 14:05:54

Input Set : A:\pbn37seq.txt

Output Set: N:\CRF3\10192001\I773307.raw

67	130	135	140	
E--> 69	ctg gag gac acg ctg cta ggc tac ctt gct gat gac ctc aca tgg tgt	480		
70	Leu Glu Asp Thr Leu Leu Gly Tyr Leu Ala Asp Asp Leu Thr Trp Cys			
71	145 150 155 160			
E--> 73	ggt gaa ttc aac act tcc aaa ata aac tat caa tct tgc cca gac tgg	528		
74	Gly Glu Phe Asn Thr Ser Lys Ile Asn Tyr Gln Ser Cys Pro Asp Trp			
75	165 170 175			
E--> 77	aga aag gac tgc agc aac aac cct gtt tca gta ttc tgg aaa acg gtt	576		
78	Arg Lys Asp Cys Ser Asn Asn Pro Val Ser Val Phe Trp Lys Thr Val			
79	180 185 190			
E--> 81	tcc cgc agg ttt gca gaa gct gcc tgt gat gtg gtc cat gtg atg ctc	624		
82	Ser Arg Arg Phe Ala Glu Ala Ala Cys Asp Val Val His Val Met Leu			
83	195 200 205			
E--> 85	aat gga tcc cgc agt aaa atc ttt gac aaa aac agc act ttt ggg agt	672		
86	Asn Gly Ser Arg Ser Lys Ile Phe Asp Lys Asn Ser Thr Phe Gly Ser			
87	210 215 220			
E--> 89	gtg gaa gtc cat aat ttg caa cca gag aag gtt cag aca cta gag gcc	720		
90	Val Glu Val His Asn Leu Gln Pro Glu Lys Val Gln Thr Leu Glu Ala			
91	225 230 235 240			
E--> 93	tgg gtg ata cat ggt gga aga gaa gat tcc aga gac tta tgc cag gat	768		
94	Trp Val Ile His Gly Gly Arg Glu Asp Ser Arg Asp Leu Cys Gln Asp			
95	245 250 255			
E--> 97	ccc acc ata aaa gag ctg gaa tgc att ata agc aaa agg aat att caa	816		
98	Pro Thr Ile Lys Glu Leu Glu Ser Ile Ile Ser Lys Arg Asn Ile Gln			
99	260 265 270			
E--> 101	ttt tcc tgc aag aat atc tac aga cct gac aag ttt ctt cag tgt gtg	864		
102	Phe Ser Cys Lys Asn Ile Tyr Arg Pro Asp Lys Phe Leu Gln Cys Val			
103	275 280 285			
E--> 105	aaa aat cct gag gat tca tct tgc aca tct gag atc tgagccagtc	910		
106	Lys Asn Pro Glu Asp Ser Ser Cys Thr Ser Glu Ile			
107	290 295 300			
E--> 109	gotgtggttg ttttagctcc ttgactcett gtggtttatg tcatcataca tgactcagca	970		
E--> 111	tacctgctgg tgcagagctg aagatttttg aggtcctcc acaataaggt caatgccaga	1030		
E--> 113	gacggaagcc tttttcccca aagtcttaaa ataacttata tcatcagcat acctttattg	1090		
E--> 115	tgatctatca atagtcaaga aaaattattg tataagatta gaatgaaaat tgtatgttaa	1150		
E--> 117	gttacttcac ttttaattctc atgtgatect tttatgttat ttatatattg gtaacatcct	1210		
E--> 119	ttctattgaa aaatcaccac accaaacctc tcttattaga acaggcaagt gaagaaaagt	1270		
E--> 121	gaatgctcaa gtttttcaga aagcattaca tttcc	1305		

nos. off

09/773,307

3

<210> 22  
<211> 66  
<212> DNA  
<213> Hominidae

*last sequence in file*

<400> 22  
ttagcgaatt ggacgacaga tgtatcctac ggtctcttga tttccttttt tgctttcttg 60

tcatag

66

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/773,307

DATE: 10/19/2001

TIME: 14:05:55

Input Set : A:\pbn37seq.txt

Output Set: N:\CRF3\10192001\I773307.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:28 M:254 E: No. of Bases conflict, LENGTH:Input:-61 Counted:45 SEQ:1  
L:28 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4  
M:254 Repeated in SeqNo=1  
L:121 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1305 Found:1411 SEQ:1  
L:13 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (23) Counted (22)